

AUTOMATED DIAGNOSTIC ANALYZER AND METHOD

This application is a divisional of Serial No. 09/303,030 filed April 30, 1999, which claims the benefit of International Application No. PCT/US99/09343 filed April 30, 1999, which in turn claims the benefit of U.S. Provisional Application No. 60/083,927 filed May 1, 1998.

1. Field of The Invention

The present invention relates to an automated analyzer for performing multiple diagnostic assays simultaneously.

2. Background of The Invention

None of the references described or referred to herein are admitted to be prior art to the claimed invention.

Diagnostic assays are widely used in clinical diagnosis and health science research to detect or quantify the presence or amount of biological antigens, cell abnormalities, disease states, and disease-associated pathogens, including parasites, fungi, bacteria and viruses present in a host organism or sample. Where a diagnostic assay permits quantification, practitioners may be better able to calculate the extent of infection or disease and to determine the state of a disease over time. In general, diagnostic assays are based either on the detection of antigens (immunoassays) or nucleic acids (nucleic acid-based assays) belonging to an organism or virus of interest.

Nucleic acid-based assays generally include several steps leading to the detection or quantification of one or more target nucleic acid sequences in a sample which are specific to the organism or virus of interest. The targeted nucleic acid sequences can also be specific to an identifiable group of organisms or viruses, where the group is defined by at least one shared sequence of nucleic acid that is common to all members of the group and is specific to that group in the sample being assayed. The detection of individual and groups of organisms and viruses using nucleic acid-based methods is fully described by Kohne, U.S. Patent No. 4,851,330, and Hogan, U.S. Patent No. 5,541,308.

The first step in a nucleic acid-based assay is designing a probe which exhibits specificity, under stringent hybridization conditions, for a nucleic acid sequence belonging to the organism or virus of interest. While nucleic acid-based assays can be designed to detect either deoxyribonucleic acid (DNA) or ribonucleic acid (RNA), ribosomal RNA (rRNA), or the gene

encoding rRNA (rDNA), is typically the preferred nucleic acid for detection of a prokaryotic or eukaryotic organism in a sample. Ribosomal RNA target sequences are preferred because of their relative abundance in cells, and because rRNA contains regions of sequence variability that can be exploited to design probes capable of distinguishing between even closely related organisms. (Ribosomal RNA is the major structural component of the ribosome, which is the situs of protein synthesis in a cell.) Viruses, which do not contain rRNA, and cellular changes are often best detected by targeting DNA, RNA, or a messenger RNA (mRNA) sequence, which is a nucleic acid intermediate used to synthesize a protein. When the focus of a nucleic acid-based assay is the detection of a genetic abnormality, then the probes are usually designed to detect identifiable changes in the genetic code, such as the abnormal Philadelphia chromosome associated with chronic myelocytic leukemia. *See, e.g., Stephenson et al., U.S. Patent No. 4,681,840.*

When performing a nucleic acid-based assay, preparation of the sample is necessary to release and stabilize target nucleic acids which may be present in the sample. Sample preparation can also serve to eliminate nuclease activity and remove or inactivate potential inhibitors of nucleic acid amplification (discussed below) or detection of the target nucleic acids. *See, e.g., Ryder et al., U.S. Patent No. 5,639,599, which discloses methods for preparing nucleic acid for amplification, including the use of complexing agents able to complex with ferric ions contributed by lysed red blood cells. The method of sample preparation can vary and will depend in part on the nature of the sample being processed (e.g., blood, urine, stool, pus or sputum). When target nucleic acids are being extracted from a white blood cell population present in a diluted or undiluted whole blood sample, a differential lysis procedure is generally followed. See, e.g., Ryder et al., European Patent Application No. 93304542.9 and European Patent Publication No. 0547267. Differential lysis procedures are well known in the art and are designed to specifically isolate nucleic acids from white blood cells, while limiting or eliminating the presence or activity of red blood cell products, such as heme, which can interfere with nucleic acid amplification or detection.*

Before or after exposing the extracted nucleic acid to a probe, the target nucleic acid can be immobilized by target-capture means, either directly or indirectly, using a "capture probe" bound to a substrate, such as a magnetic bead. Examples of target-capture methodologies are described by Ranki *et al.*, U.S. Patent No. 4,486,539, and Stabinsky, U.S. Patent No. 4,751,177. Target capture probes are generally short sequences of nucleic acid (*i.e.*, oligonucleotide)

capable of hybridizing, under stringent hybridization conditions, with a sequence of nucleic acid which also contains the target sequence. Magnets in close proximity to the reaction vessel are used to draw and hold the magnetic beads to the side of the vessel. Once the target nucleic acid is thus immobilized, the hybridized nucleic acid can be separated from non-hybridized nucleic acid by aspirating fluid from the reaction vessel and optionally performing one or more wash steps.

In most instances, it is desirable to amplify the target sequence using any of several nucleic acid amplification procedures which are well known in the art. Specifically, nucleic acid amplification is the enzymatic synthesis of nucleic acid amplicons (copies) which contain a sequence that is complementary to a nucleic acid sequence being amplified. Examples of nucleic acid amplification procedures practiced in the art include the polymerase chain reaction (PCR), strand displacement amplification (SDA), ligase chain reaction (LCR), and transcription-associated amplification (TAA). Nucleic acid amplification is especially beneficial when the amount of target sequence present in a sample is very low. By amplifying the target sequences and detecting the amplicon synthesized, the sensitivity of an assay can be vastly improved, since fewer target sequences are needed at the beginning of the assay to better ensure detection of nucleic acid in the sample belonging to the organism or virus of interest.

Methods of nucleic acid amplification are thoroughly described in the literature. PCR amplification, for instance, is described by Mullis *et al.* in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, and in *Methods in Enzymology*, 155:335-350 (1987). Examples of SDA can be found in Walker, *PCR Methods and Applications*, 3:25-30 (1993), Walker *et al.* in *Nucleic Acids Res.*, 20:1691-1996 (1992) and *Proc. Natl. Acad. Sci.*, 89:392-396 (1991). LCR is described in U.S. Patent Nos. 5,427,930 and 5,686,272. And different TAA formats are provided in publications such as Burg *et al.* in U.S. Patent No. 5,437,990; Kacian *et al.* in U.S. Patent Nos. 5,399,491 and 5,554,516; and Gingeras *et al.* in International Application No. PCT/US87/01966 and International Publication No. WO 88/01302, and International Application No. PCT/US88/02108 and International Publication No. WO 88/10315.

Detection of a targeted nucleic acid sequence requires the use of a probe having a nucleotide base sequence which is substantially complementary to the targeted sequence or, alternatively, its amplicon. Under selective assay conditions, the probe will hybridize to the targeted sequence or its amplicon in a manner permitting a practitioner to detect the presence of the targeted sequence in a sample. Effective probes are designed to prevent non-specific